Keratinocyte Derived Interferon

```
   1 CCA CGC GTC CGG GAT TTT TTA GCT TGC AAA AAA AAT GAG CAC CAA ACC TGA TAT GAT TCA 60
   1                                             M   S   T   K   P   D   M   I   Q  9

  61 AAA GTG TTT GTG GCT TGA GAT CCT TAT GGG TAT ATT CAT TGC TGG CAC CCT ATC CCT GGA 120
  10  K   C   L   W   L   E   I   L   M   G   I   F   I   A   G   T   L   S   L   D 29

 121 CTG TAA CTT ACT GAA CGT TCA CCT GAG AAG AGT CAC CTG GCA AAA TCT GAG ACA TCT GAG 180
  30   C   N   L   L   N   V   H   L   R   R   V   T   W   Q   N   L   R   H   L   S 49

 181 TAG TAT GAG CAA TTC ATT TCC TGT AGA ATG TCT ACG AGA AAA CAT AGC TTT TGA GTT GCC 240
  50   S   M   S   N   S   F   P   V   E   C   L   R   E   N   I   A   F   E   L   P 69

 241 CCA AGA GTT TCT GCA ATA CAC CCA ACC TAT GAA GAG GGA CAT CAA GAA GGC CTT CTA TGA 300
  70   Q   E   F   L   Q   Y   T   Q   P   M   K   R   D   I   K   K   A   F   Y   E 89

 301 AAT GTC CCT ACA GGC CTT CAA CAT CTT CAG CCA ACA CAC CTT CAA ATA TTG GAA AGA GAG 360
  90   M   S   L   Q   A   F   N   I   F   S   Q   H   T   F   K   Y   W   K   E   R 109

 361 ACA CCT CAA ACA AAT CCA AAT AGG ACT TGA TCA GCA AGC AGA GTA CCT GAA CCA ATG CTT 420
 110   H   L   K   Q   I   Q   I   G   L   D   Q   Q   A   E   Y   L   N   Q   C   L 129

 421 GGA GGA AGA CGA GAA TGA AAA TGA AGA CAT GAA AGA AAT GAA AGA GAA TGA GAT GAA ACC 480
 130   E   E   D   E   N   E   N   E   D   M   K   E   M   K   E   N   E   M   K   P 149

 481 CTC AGA AGC CAG GGT CCC CCA GCT GAG CAG CCT GGA ACT GAG GAG ATA TTT CCA CAG GAT 540
 150   S   E   A   R   V   P   Q   L   S   S   L   E   L   R   R   Y   F   H   R   I 169

 541 AGA CAA TTT CCT GAA AGA AAA GAA ATA CAG TGA CTG TGC CTG GGA GAT TGT CCG AGT GGA 600
 170   D   N   F   L   K   E   K   K   Y   S   D   C   A   W   E   I   V   R   V   E 189

 601 AAT CAG AAG ATG TTT GTA TTA CTT TTA CAA ATT TAC AGC TCT ATT CAG GAG GAA ATA AGA 660
 190   I   R   R   C   L   Y   Y   F   Y   K   F   T   A   L   F   R   R   K   *     207

 661 ATC ATC TAC CTT CAA GCA AGA ATT AAC AGA GAT TGT GGC TAC GCA AAT GCA CCA AAA AAG 720
 721 GGT GAA ATA TAT CTG AAA TGT ACC TGG TTC TGC CCT TGG AAG CCA CTT CCT GCT CAT GCC 780
 781 ACT AAC AGC ATG CTG CCA AAC TGT TCA GAT TCA AGA TTA TTC CAA GCG CAG GGC CCA AAT 840
 841 GTT ATA GCC AAA GAA AGT CTT ATG ATA AAA GTG AGG CAA ATT TCA GCC AAG AAG TTA GAA 900
 901 GAG ATG TTT AAA AGA ACA AGA ACA AAT TGT GGA TCA TGG TAT ATG CAG GCT ATC AGC AGA 960
 961 AGG ATC AGA CAA TAA AAT GAG TTA GTG CAA ACC ATT TAG TAA AAA TAA CTA TCA GCA GAG 1020
1021 TTG TTC CAG ATT AAA AAT AGT ACT ACA AGC TTG TAA AGG AGT TAG GAC ATG CAA GCT ACT 1080
1081 GAG CAT AAA ATA TAT ACT TGC TAT TTT TCA TGA CTT TCT CTA ATA AAG TCT TTG ACT GTT 1140
1141 CTC TCT AAT AAA AAA AAA AAA AAA AAA AAA 1170
```


FIG. 1

```
HKAPI15      10 KCLWLEILMGIFIAG...TLSLDCNLLNVH..LRRVTWQNLRHLSSMSNS 54
                ..|:.:| :.:.:.    . ||:|:| . |  |.| |:  |:::..:|
INF-omega     1 MALLFPLLAALVMTSYSPVGSLGCDLPQNHGLLSRNTLVLLHQMRRIS.. 48

HKAPI15      55 FPVECLRENIAFELPQEFLQYTQPMKRDIKKAFYEMSLQAFNIF.SQHTF 103
                 |. ||:.. .| :|||:.. .|  | .:...:.||  | |.:| .:.. 
INF-omega    49 .PFLCLKDRRDFRFPQEMVKGSQLQKAHVMSVLHEMLQQIFSLFHTERSS 97

HKAPI15     104 KYWKERHLKQIQIGLDQQAEYLNQCLEEDENENEDMKEMKENEMKPSEAR 153
                   |.   |.|:.:|.|| :.|: || :  .|.|.  .:..
INF-omega    98 AAWNMTLLDQLHTELHQQLQHLETCLLQVVGEGESAGAISS......... 138

HKAPI15     154 VPQLSSLELRRYFHRIDNFLKEKKYSDCAWEIVRVEIRRCLYYFYKFTAL 203
                    ..|.|||||: |  :||||||||||||:||:||.:.:|:.  .: .
INF-omega   139 ....PALTLRRYFQGIRVYLKEKKYSDCAWEVVRMEIMKSLFLSTNMQER 184

HKAPI15     204 FRRK 207
                :|.|
INF-omega   185 LRSK 188
```

FIG. 2

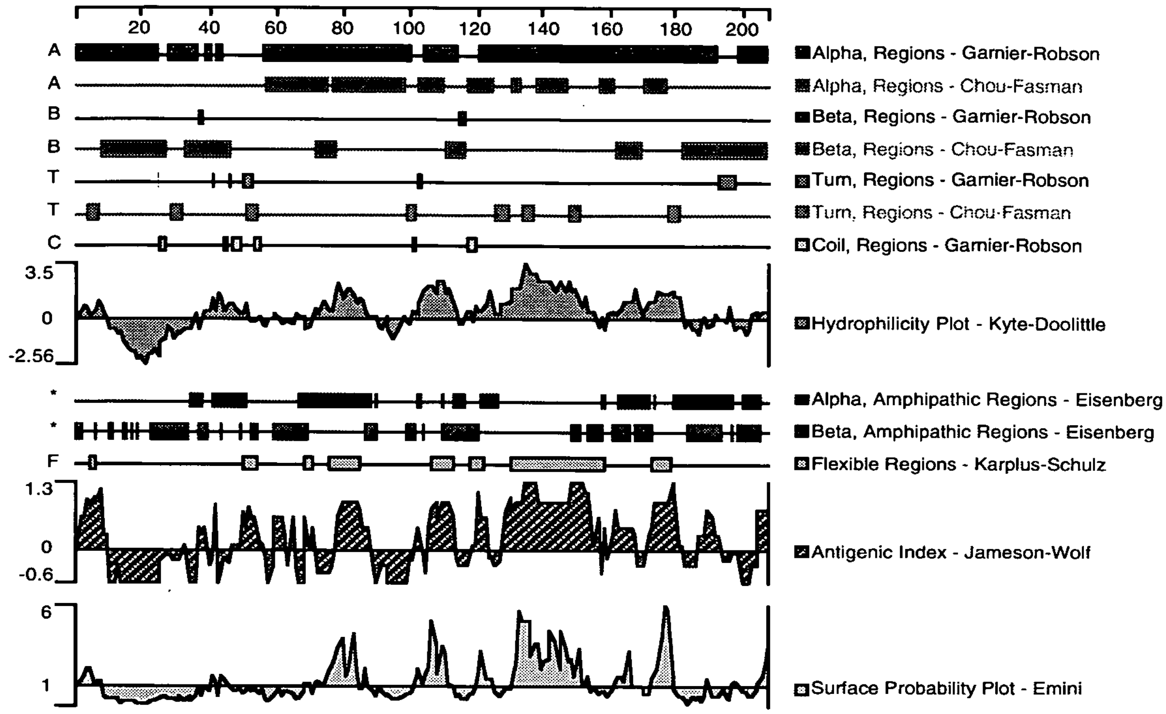


FIG. 3

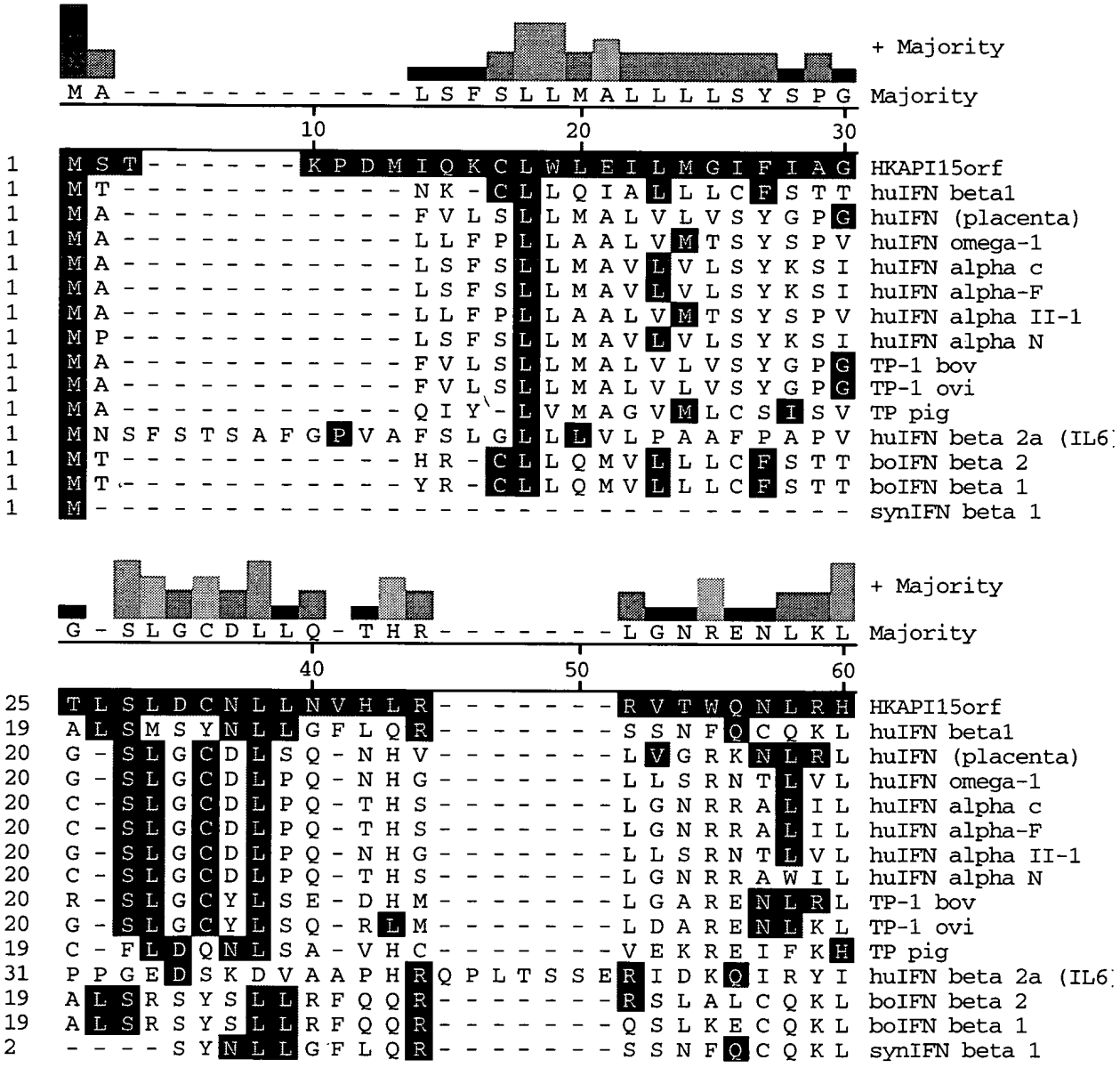
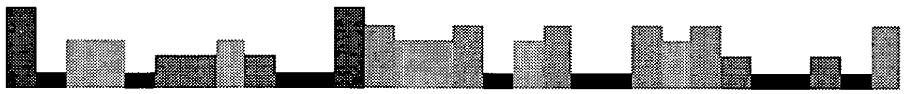
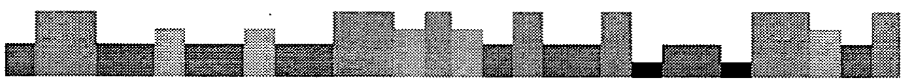


FIG. 4A



+ Majority

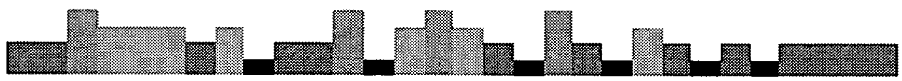
```
     L A Q M N R I S P H S C L K D R M D F G F P Q E M V Q G N Q  Majority
                        70                  80                  90
48   L S S M S N S F P V E C L R E N I A F E L P Q E F L Q Y T Q  HKAPI15orf
42   L W Q L N G R L E Y - C L K D R M N F D I P E E I K Q L Q Q  huIFN beta1
41   L D E M R R L S P H F C L Q D R K D F A L P Q E M V E G G Q  huIFN (placenta)
41   L H Q M R R I S P F L C L K D R R D F R F P Q E M V K G S Q  huIFN omega-1
41   L G Q M G R I S P F S C L K D R H D F R I P Q E E F D G N Q  huIFN alpha c
41   L A Q M G R I S P F S C L K D R H D F G F P Q E E F D G N Q  huIFN alpha-F
41   L H Q M R R I S P F L C L K D R R D F R F P Q E M V K G S Q  huIFN alpha II-1
41   L A Q M G R I S H F S C L K D R Y D F G F P Q E V F D G N Q  huIFN alpha N
41   L A R M N R L S P H P C L Q D R K D F G L P Q E M V E G N Q  TP-1 bov
41   L E P M N R L S P H S C L Q D R K D F G L P Q E M V E G D Q  TP-1 ovi
40   L Q E I K K I P S Q L C L K D R I D F K F P W K R E S I T Q  TP pig
61   L D G I S A L R K E T C N K S N M C - - - - - E S S K E A L  huIFN beta 2a (IL6
42   L R Q L P S T P Q H - C L E A R M D F Q M P E E M K Q A Q Q  boIFN beta 2
42   L G Q L P S T S Q H - C L E A R M D F Q M P E E M K Q E Q Q  boIFN beta 1
21   L W Q L N G R L E Y - C L K D R M N F D I P E E I K Q L Q Q  synIFN beta 1
```



+ Majority

```
     F Q K A Q A I S V L H E M L Q Q I F N L F S T E D S S A A W  Majority
                       100                 110                 120
78   P M K R D I K K A F Y E M S L Q A F N I F S - Q H T F K Y W  HKAPI15orf
71   F Q K E D A A L T I Y E M L Q N I F A I F R Q D S S S T G W  huIFN beta1
71   L Q E A Q A I S V L H E M L Q Q S F N L F H T E H S S A A W  huIFN (placenta)
71   L Q K A H V M S V L H E M L Q Q I F S L F H T E R S S A A W  huIFN omega-1
71   F Q K A Q A I S V L H E M I Q Q T F N L F S T E D S S A A W  huIFN alpha c
71   F Q K A Q A I S V L H E M I Q Q T F N L F S T K D S S A T W  huIFN alpha-F
71   L Q K A H V M S V L H E M L Q Q I F S L F H T E R S S A A W  huIFN alpha II-1
71   F Q K A Q A I S A F H E M I Q Q T F N L F S T K D S S A A W  huIFN alpha N
71   L Q K D Q A I S V L H E M L Q Q C F N L F Y T E H S S A A W  TP-1 bov
71   L Q K D Q A F P V L Y E M L Q Q T F N L F H T E H S S A A W  TP-1 ovi
70   I Q K T E G T C Y C Y L M L Q Q I S G V F S K K D S R A A W  TP pig
86   A E N N L N L P K M A E K - D G C F Q S G F N E E T C L V K  huIFN beta 2a (IL6
71   F Q K E D A I L V I Y E M L Q Q I F N I L T R D F S S T G W  boIFN beta 2
71   F Q K E D A I L V M Y E V L Q H I F G I L T R D F S S T G W  boIFN beta 1
50   F Q K E D A A L T I Y E M L Q N I F A I F R Q D S S S T G W  synIFN beta 1
```

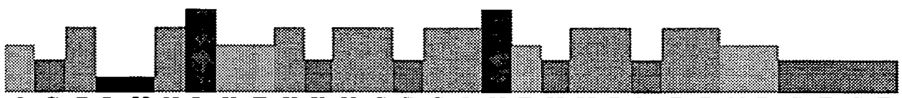
FIG. 4B



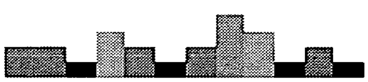

```
                                                                                  Majority
    N E T L L E Q L L T E L Y Q Q L N D L E A C L E Q V M G E E                  Majority
                      130                           140                        150
107 K E R H L K Q I Q I G L D Q Q A E Y L N Q C L E E D E N E N   HKAPI15orf
101 N E T I V E N L L A N V Y H Q I N H L K T V L E E K L E K E   huIFN beta1
101 D T T L L E P C R T G L H Q Q L D N L D A C L G Q V M G E E   huIFN (placenta)
101 N M T L L D Q L H T G L H Q Q L Q H L E T C L L Q V V G E G   huIFN omega-1
101 E Q S L L E K F S T E L Y Q Q L N D L E A C V I Q E V G V E   huIFN alpha c
101 E Q S L L E K F S T E L N Q Q L N D L E A C V I Q E V G V E   huIFN alpha-F
101 N M T L L D Q L H T E L H Q Q L Q H L E T C L L Q V V G E G   huIFN alpha II-1
101 D E T L L D K F Y I E L F Q Q L N D L E A C V T Q E V G V E   huIFN alpha N
101 N T T L L E Q L C T G L Q Q Q L E D L D A C L G P V M G E K   TP-1 bov
101 D T T L L E Q L C T G L Q Q Q L E D L D T C R G Q V M G E E   TP-1 ovi
100 N T T L L D Q L L S S L D L G L R R L E - - - - - H M K K D   TP pig
115 I I T G L L E F E V Y L E Y L Q N R F E S S E E Q A R A V Q   huIFN beta 2a (IL6
101 S E T I I E D L L E E L Y E Q M N H L E P I Q K E I M Q K Q   boIFN beta 2
101 S E T I I E D L L K E L Y W Q M N R L Q P I Q K E I M Q K Q   boIFN beta 1
80  N E T I V E N L L A N V Y H Q I N H L K T V L E E K L E K E   synIFN beta 1
```


```
    E S - - - - - - - - - - - - - A L G N V D S I L A L R K Y F   Majority
                      160                           170                        180
137 E D M K E M K E N E M K P S E A R V P Q L S S L E L R R Y F   HKAPI15orf
131 D F - - - - - - - - - - - - - T R G K L M S S L H L K R Y Y   huIFN beta1
131 D S - - - - - - - - - - - - - A L G R T G P T L A L K R Y F   huIFN (placenta)
131 E S - - - - - - - - - - - - - A G A I S S P A L T L R R Y F   huIFN omega-1
131 E T - - - - - - - - - - - - - P L M N E D S I L A V R K Y F   huIFN alpha c
131 E T - - - - - - - - - - - - - P L M N V D S I L A V K K Y F   huIFN alpha-F
131 E S - - - - - - - - - - - - - A G A I S S P A L T L R R Y F   huIFN alpha II-1
131 E I - - - - - - - - - - - - - A L M N E D S I L A V R K Y F   huIFN alpha N
131 D S - - - - - - - - - - - - - D M G R M G P I L T V K K Y F   TP-1 bov
131 D S - - - - - - - - - - - - - E L G N M D P I V T V K K Y F   TP-1 ovi
125 N M - - - - - - - - - - - - - D C P H V G S A L - - R K Y F   TP pig
145 M S T K V L I Q F L Q K K A K N L D A I T T P D P T T N - -   huIFN beta 2a (IL6
131 N S - - - - - - - - - - - - - T M G D - T T V L H L R K Y Y   boIFN beta 2
131 N S - - - - - - - - - - - - - T T E D - T I V P H L G K Y Y   boIFN beta 1
110 D F - - - - - - - - - - - - - T R G K L M S S L H L K R Y Y   synIFN beta 1
```

FIG. 4C



```
                                                                           + Majority
    Q G I L V Y L K E K K Y S D C A W E V V R V E I M R S F S F   Majority
                      190                           200                           210
167 H R I D N F L K E K K Y S D C A W E I V R V E I R R C L Y Y   HKAPI15orf
148 G R I L H Y L K A K E Y S H C A W T I V R V E I L R N F Y F   huIFN beta1
148 Q G I H V Y L K E K G Y S D C A W E T V R L E I M R S F S S   huIFN (placenta)
148 Q G I R V Y L K E K K Y S D C A W E V V R M E I M K S L F L   huIFN omega-1
148 Q R I T L Y L I E R K Y S P C A W E V V R A E I M R S L S F   huIFN alpha c
148 Q R I T L Y L T E K K Y S P C A W E V V R A E I M R S F S L   huIFN alpha-F
148 Q G I R V Y L K E K K Y S D C A W E V V R M E I M K S L F L   huIFN alpha II-1
148 Q R I T L Y L M G K K Y S P C A W E V V R A E I M R S F S F   huIFN alpha N
148 Q G I H V Y L K E K E Y S D C A W E I I R M E M M R A L S S   TP-1 bov
148 Q G I Y D Y L Q E K G Y S D C A W E I V R V E M M R A L T V   TP-1 ovi
140 Q G I Q L Y L K E K K Y S P C A W E I V R V E I E R C F S L   TP pig
173 A S L L T K L Q A Q N - - - - Q W - - - - L Q D M T T H L I   huIFN beta 2a (IL6
147 F N L V Q Y L K S K E Y N R C A W T V V R V Q I L R N F S F   boIFN beta 2
147 F N L M Q Y L E S K E Y D R C A W T V V Q V Q I L T N V S F   boIFN beta 1
127 G R I L H Y L K A K E Y S H C A W T I V R V E I L R N F Y F   synIFN beta 1
```



```
                                                                           + Majority
    S T N L Q E R L R R K D - - - - - -                           Majority
                      220
197 F Y K F T A L F R R K                                         HKAPI15orf
178 I N R L T G Y L R N                                           huIFN beta1
178 L I S L Q E R L R M M D G D L S S P                           huIFN (placenta)
178 S T N M Q E R L R S K D R D L G S S                           huIFN omega-1
178 S T N L Q K R L R R K D                                       huIFN alpha c
178 S K I F Q E R L R R K E                                       huIFN alpha-F
178 S T N M Q E R L R S K D R D L G S S                           huIFN alpha II-1
178 S T N L Q K G L R R K D                                       huIFN alpha N
178 S T T L Q K R L R K M G G D L N S L                           TP-1 bov
178 S T T L Q K R L T K M G G D L N S P                           TP-1 ovi
170 T                                                             TP pig
195 L R S F K E F L Q S S L R A L R Q M                           huIFN beta 2a (IL6
177 L T R L T G Y L R E                                           boIFN beta 2
177 L M R L T G Y V R D                                           boIFN beta 1
157 I N R L T G Y L G N                                           synIFN beta 1
```

FIG. 4D

```
                10        20        30        40
1    CTGGACTGTAACTTACTGAACGTTCACCTGAGAAGAGTCA wt KDI orf
1    CTGGATTGCAACCTGCTGAACGTTCATCTGCGTCGCGTGA s KDI orf

                50        60        70        80
41   CCTGGCAAAATCTGAGACATCTGAGTAGTATGAGCAATTC wt KDI orf
41   CCTGGCAGAACCTGCGTCACCTGAGCTCTATGAGCAACTC s KDI orf

                90       100       110       120
81   ATTTCCTGTAGAATGTCTACGAGAAAACATAGCTTTTGAG wt KDI orf
81   CTTCCCGGTTGAGTGCCTGCGTGAAAACATCGCGTTTGAA s KDI orf

               130       140       150       160
121  TTGCCCCAAGAGTTTCTGCAATACACCCAACCTATGAAGA wt KDI orf
121  CTGCCGCAAGAATTCCTGCAATACACCCAGCCGATGAAAC s KDI orf

               170       180       190       200
161  GGGACATCAAGAAGGCCTTCTATGAAATGTCCCTACAGGC wt KDI orf
161  GTGATATCAAGAAAGCGTTCTACGAAATGTCCCTGCAGGC s KDI orf

               210       220       230       240
201  CTTCAACATCTTCAGCCAACACACCTTCAAATATTGGAAA wt KDI orf
201  GTTCAACATCTTCAGCCAGCACACCTTCAAATACTGGAAA s KDI orf

               250       260       270       280
241  GAGAGACACCTCAAACAAATCCAAATAGGACTTGATCAGC wt KDI orf
241  GAACGTCACCTGAAACAGATCCAGATCGGTCTGGATCAGC s KDI orf

               290       300       310       320
281  AAGCAGAGTACCTGAACCAATGCTTGGAGGAAGACGAGAA wt KDI orf
281  AAGCAGAATACCTGAACCAGTGCCTGGAAGAAGACGAGAA s KDI orf

               330       340       350       360
321  TGAAAATGAAGACATGAAAGAAATGAAAGAGAATGAGATG wt KDI orf
321  CGAAAACGAAGACATGAAAGAAATGAAAGAGAACGAAATG s KDI orf

               370       380       390       400
361  AAACCCTCAGAAGCCAGGGTCCCCCAGCTGAGCAGCCTGG wt KDI orf
361  AAACCGTCTGAAGCGCGTGTTCCGCAGCTGAGCTCTCTGG s KDI orf

               410       420       430       440
401  AACTGAGGAGATATTTCCACAGGATAGACAATTTCCTGAA wt KDI orf
401  AACTGCGCCGTTACTTCCACCGCATCGACAACTTCCTGAA s KDI orf

               450       460       470       480
441  AGAAAAGAAATACAGTGACTGTGCCTGGGAGATTGTCCGA wt KDI orf
441  AGAAAAGAAATACTCTGACTGCGCGTGGGAAATCGTGCGT s KDI orf

               490       500       510       520
481  GTGGAAATCAGAAGATGTTTGTATTACTTTTACAAATTTA wt KDI orf
481  GTGGAAATCCGCCGTTGTCTGTACTACTTCTACAAATTCA s KDI orf

               530       540
521  CAGCTCTATTCAGGAGGAAA                     wt KDI orf
521  CCGCTCTGTTCCGTCGCAAA                     s KDI orf
```

FIG. 5

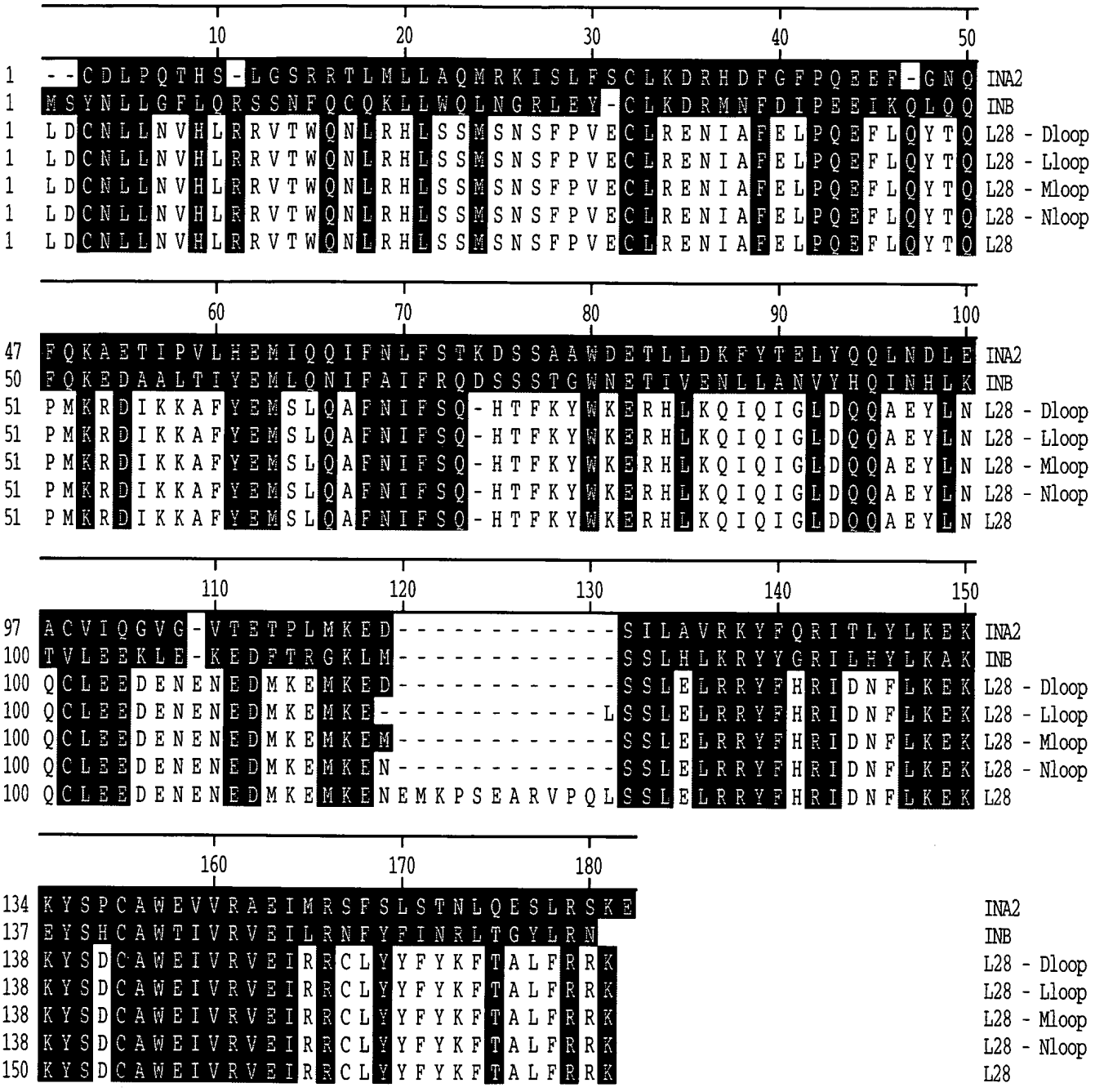


FIG. 6